



SEQUENCE LISTING

<110> Pagano, M.

<120> METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS

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<140> 10/042,417

<141> 2002-01-07

<150> 60/260,179

<151> 2001-01-05

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<170> PatentIn Ver. 2.0

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Glu Thr Leu Leu Lys Arg Asp Phe Leu Lys Leu Leu Pro Leu Glu Leu
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Ile Leu Trp Arg Tyr Phe Leu Leu Arg Asp Leu Pro Ser Trp Ser Ser
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Val Asp Trp Lys Ser Leu Pro Tyr Leu Gln Ile Leu Lys Lys Pro Ile
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 <213> Homo sapiens

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 <213> Homo sapiens

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 35 40 45
 Cys Asp Phe Asn Cys Asn His Val His Ser Gly Leu Lys Leu Val Lys
 50 55 60
 Pro Asp Asp Ile Gly Arg Leu Val Ser Tyr Thr Pro Ala Tyr Leu Glu
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<212> DNA
<213> Homo sapiens

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<211> 338
<212> PRT
<213> Homo sapiens

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Arg Pro Gln Arg Gly Pro Gly Pro Gly Gly Ser Gln Ala Met Asp Ala
35 40 45
Pro His Ser Lys Ala Ala Leu Asp Ser Ile Asn Glu Leu Pro Asp Asn
50 55 60

Ile	Leu	Leu	Glu	Leu	Phe	Thr	His	Val	Pro	Ala	Arg	Gln	Leu	Leu	Leu	65	70	75	80
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Trp	Asp	Gln	Pro	Val	Ala	Asp	Trp	Lys	Ile	Phe	Tyr	Phe	Leu	Arg	Ser	115	120	125	
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Ala	Trp	Gln	Ile	Asp	Phe	Asn	Gly	Gly	Asp	Arg	Trp	Lys	Val	Asp	Ser	145	150	155	160
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Ser	Phe	Val	Thr	Ser	Tyr	Glu	Leu	Cys	Leu	Lys	Trp	Glu	Leu	Val	Asp	180	185	190	
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Arg	Tyr	Ile	Leu	Phe	Gln	His	Gly	Gly	Arg	Asp	Thr	Gln	Tyr	Trp	Ala	275	280	285	
Gly	Trp	Tyr	Gly	Pro	Arg	Val	Thr	Asn	Ser	Ser	Ile	Val	Val	Ser	Pro	290	295	300	
Lys	Met	Thr	Arg	Asn	Gln	Ala	Ser	Ser	Glu	Ala	Gln	Pro	Gly	Gln	Lys	305	310	315	320
His	Gly	Gln	Glu	Glu	Ala	Ala	Gln	Ser	Pro	Tyr	Gly	Ala	Val	Val	Gln	325	330	335	
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<210> 13
 <211> 1763
 <212> DNA
 <213> Homo sapiens
 <400> 13

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1763

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<210> 14
 <211> 482
 <212> PRT
 <213> Homo sapiens

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<400> 14
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Leu Ile Cys Leu Ile Leu His Asp Asp Ile Pro Pro Pro Asn Ile Pro
      35              40              45

Ser Ser Thr Asp Ser Glu His Ser Ser Leu Gln Asn Asn Glu Gln Pro
      50              55              60

Ser Leu Ala Thr Ser Ser Asn Gln Thr Ser Ile Gln Asp Glu Gln Pro
      65              70              75              80

Ser Asp Ser Phe Gln Gly Gln Ala Ala Gln Ser Gly Val Trp Asn Asp
      85              90              95

Asp Ser Met Leu Gly Pro Ser Gln Asn Phe Glu Ala Glu Ser Ile Gln
      100              105              110

Asp Asn Ala His Met Ala Glu Gly Thr Gly Phe Tyr Pro Ser Glu Pro
      115              120              125

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Pro Gly Pro Asn Pro Ile Leu Pro Gly Arg Gly Gly Pro Asn Asp Arg
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Phe Met

<210> 15
 <211> 43
 <212> PRT
 <213> Homo sapiens

<400> 15
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<210> 16
 <211> 40
 <212> PRT
 <213> Homo sapiens

<400> 16
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<210> 17
 <211> 39
 <212> PRT
 <213> Homo sapiens

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His Met Pro Asp Leu Trp Arg
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<210> 18
 <211> 39

<212> PRT
 <213> Homo sapiens
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 <211> 39
 <212> PRT
 <213> Homo sapiens
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 <211> 40
 <212> PRT
 <213> Homo sapiens
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 20 25 30
 Ile Asp Leu Leu Thr Leu Trp Lys
 35 40

<210> 21
 <211> 39
 <212> PRT
 <213> Homo sapiens
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 20 25 30
 Asn Asp Pro Leu Leu Trp Arg
 35

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<400> 22
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<212> DNA
<213> Homo sapiens
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<210> 24
<211> 434
<212> PRT
<213> Homo sapiens
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      20             25             30

Thr His Thr His Thr Val Leu Leu Asp Trp Gly Ser Leu Pro His His
      35             40             45

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Ala Leu Gly Leu Ser Lys Cys Glu Val Ser Cys Ser Ala Phe Ile Arg
 370 375 380

Phe Val Arg Leu Cys Glu Arg Arg Leu Thr Gln Leu Ser Val Met Glu
 385 390 395 400

Glu Val Leu Ile Pro Asp Glu Asp Tyr Ser Leu Asp Glu Ile His Thr
 405 410 415

Glu Val Ser Lys Tyr Leu Gly Arg Val Trp Phe Pro Asp Val Met Pro
 420 425 430

Leu Trp

<210> 25
 <211> 1970
 <212> DNA
 <213> Homo sapiens

<400> 25
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 <211> 634
 <212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> all Xaa positions

<223> Xaa=unknown amino acid residue

<400> 26

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20 25 30

Val Thr Ser Thr Gly Val Asp Lys Ser Leu Asn Gln Leu Leu His Gly
35 40 45

Leu Gly Thr Ser Ser Arg Leu Ser His Phe Pro Phe Gly Lys Ser Pro
50 55 60

Pro Arg Gly Gln Phe Val Ala Ala Ala Val Glu Ile Ala Gly Arg Ser
65 70 75 80

Gly Leu Gln Met Gly Gln Gly Leu Trp Arg Val Val Arg Asn Gln Gln
85 90 95

Leu Gln Gln Glu Gly Tyr Ser Glu Gln Gly Tyr Leu Thr Arg Glu Gln
100 105 110

Ser Arg Arg Met Ala Ala Ser Asn Ile Ser Asn Thr Asn His Arg Lys
115 120 125

Gln Val Gln Gly Gly Ile Asp Ile Tyr His Leu Leu Lys Ala Arg Lys
130 135 140

Ser Lys Glu Gln Glu Gly Phe Ile Asn Leu Glu Met Leu Pro Pro Glu
145 150 155 160

Leu Ser Phe Thr Ile Leu Ser Tyr Leu Asn Ala Thr Asp Leu Cys Leu
165 170 175

Ala Ser Cys Val Trp Gln Asp Leu Ala Asn Asp Glu Leu Leu Trp Gln
180 185 190

Gly Leu Cys Lys Ser Thr Trp Gly His Cys Ser Ile Tyr Asn Lys Asn
195 200 205

Pro Pro Leu Gly Phe Ser Phe Arg Lys Xaa Tyr Met Gln Leu Asp Glu
210 215 220

Gly Ser Leu Thr Phe Asn Ala Asn Pro Asp Glu Gly Val Asn Tyr Phe
225 230 235 240

Met Ser Lys Gly Ile Leu Asp Asp Ser Pro Lys Glu Ile Ala Lys Phe
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Ile Phe Cys Thr Arg Thr Leu Asn Trp Lys Lys Leu Arg Ile Tyr Leu
260 265 270

Asp Glu Arg Arg Asp Val Leu Asp Asp Leu Val Thr Leu His Asn Phe

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Tyr	Phe	Ile	Val	Lys	Ile	Leu	Thr	Lys	Val	Phe	Pro	Phe	Leu	Ser	Asn
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Ser	Asp	Phe	Arg	Gln	Lys	Pro	Ile	Pro	Ala	Ser	Phe	Ser	Phe	Lys	Leu
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Arg	Val	Leu	Ile	Cys	Tyr	Tyr	Ile	Thr	Met	Gln	Asn	Trp	Gln	Leu	Phe
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Leu	Tyr	Lys	Phe	Ile	Ile	Phe	Phe	Ile	Leu	Lys	Thr	Gly	Leu	Ile	Lys
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Ser Glu Asn Lys Ile Xaa Leu Glu Leu Trp
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<211> 4168
<212> DNA
<213> Homo sapiens

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<210> 28
<211> 621
<212> PRT
<213> Homo sapiens

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<400> 28
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Ala Glu Glu Ala Ala Pro Glu Val Ala Gly Leu Ser Cys Leu Val Asn
      20              25              30

Leu Pro Gly Glu Val Leu Glu Tyr Ile Leu Cys Cys Gly Ser Leu Thr
      35              40              45

Ala Ala Asp Ile Gly Arg Val Ser Ser Thr Cys Arg Arg Leu Arg Glu
      50              55              60

Leu Cys Gln Ser Ser Gly Lys Val Trp Lys Glu Gln Phe Arg Val Arg
      65              70              75              80

Trp Pro Ser Leu Met Lys His Tyr Ser Pro Thr Asp Tyr Val Asn Trp
      85              90              95

Leu Glu Glu Tyr Lys Val Arg Gln Lys Ala Gly Leu Glu Ala Arg Lys
      100             105             110

Ile Val Ala Ser Phe Ser Lys Arg Phe Phe Ser Glu His Val Pro Cys
      115             120             125

Asn Gly Phe Ser Asp Ile Glu Asn Leu Glu Gly Pro Glu Ile Phe Phe
      130             135             140

Glu Asp Glu Leu Val Cys Ile Leu Asn Met Glu Gly Arg Lys Ala Leu
      145             150             155             160

Thr Trp Lys Tyr Tyr Ala Lys Lys Ile Leu Tyr Tyr Leu Arg Gln Gln

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Glu	Ser	Tyr	Leu	Glu	Gly	Ala	Val	Tyr	Ile	Asp	Gln	Tyr	Cys	Asn	Pro				
		195					200					205							
Leu	Ser	Asp	Ile	Ser	Leu	Lys	Asp	Ile	Gln	Ala	Gln	Ile	Asp	Ser	Ile				
	210					215					220								
Val	Glu	Leu	Val	Cys	Lys	Thr	Leu	Arg	Gly	Ile	Asn	Ser	Arg	His	Pro				
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Ser	Leu	Ala	Phe	Lys	Ala	Gly	Glu	Ser	Ser	Met	Ile	Met	Glu	Ile	Glu				
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Leu	Gln	Ser	Gln	Val	Leu	Asp	Ala	Met	Asn	Tyr	Val	Leu	Tyr	Asp	Gln				
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Leu	Lys	Phe	Lys	Gly	Asn	Arg	Met	Asp	Tyr	Tyr	Asn	Ala	Leu	Asn	Leu				
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Tyr	Met	His	Gln	Val	Leu	Ile	Arg	Arg	Thr	Gly	Ile	Pro	Ile	Ser	Met				
	290					295					300								
Ser	Leu	Leu	Tyr	Leu	Thr	Ile	Ala	Arg	Gln	Leu	Gly	Val	Pro	Leu	Glu				
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Pro	Val	Asn	Phe	Pro	Ser	His	Phe	Leu	Leu	Arg	Trp	Cys	Gln	Gly	Ala				
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Glu	Gly	Ala	Thr	Leu	Asp	Ile	Phe	Asp	Tyr	Ile	Tyr	Ile	Asp	Ala	Phe				
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Gly	Lys	Gly	Lys	Gln	Leu	Thr	Val	Lys	Glu	Cys	Glu	Tyr	Leu	Ile	Gly				
		355				360						365							
Gln	His	Val	Thr	Ala	Ala	Leu	Tyr	Gly	Val	Val	Asn	Val	Lys	Lys	Val				
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Leu	Gln	Arg	Met	Val	Gly	Asn	Leu	Leu	Ser	Leu	Gly	Lys	Arg	Glu	Gly				
385					390					395					400				
Ile	Asp	Gln	Ser	Tyr	Gln	Leu	Leu	Arg	Asp	Ser	Leu	Asp	Leu	Tyr	Leu				
				405					410					415					
Ala	Met	Tyr	Pro	Asp	Gln	Val	Gln	Leu	Leu	Leu	Leu	Gln	Ala	Arg	Leu				
			420					425					430						
Tyr	Phe	His	Leu	Gly	Ile	Trp	Pro	Glu	Lys	Val	Leu	Asp	Ile	Leu	Gln				
		435					440					445							
His	Ile	Gln	Thr	Leu	Asp	Pro	Gly	Gln	His	Gly	Ala	Val	Gly	Tyr	Leu				
	450					455					460								
Val	Gln	His	Thr	Leu	Glu	His	Ile	Glu	Arg	Lys	Lys	Glu	Glu	Val	Gly				
465					470					475					480				
Val	Glu	Val	Lys	Leu	Arg	Ser	Asp	Glu	Lys	His	Arg	Asp	Val	Cys	Tyr				

Ser Asn Leu Ala Glu Val Val Glu Arg Val Leu Thr Phe Leu Pro Ala
 35 40 45

Lys Ala Leu Leu Arg Val Ala Cys Val Cys Arg Leu Trp Arg Glu Cys
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Val Arg Arg Val Leu Arg Thr His Arg Ser Val Thr Trp Ile Ser Ala
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Gly Leu Ala Glu Ala Gly His Leu Xaa Gly His
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 <211> 592
 <212> DNA
 <213> Homo sapiens

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 <211> 197
 <212> PRT
 <213> Homo sapiens

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 Pro Pro Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro Pro Pro Pro Pro
 35 40 45
 Pro Pro Pro Leu Pro Gln Glu Arg Asn Asn Val Gly Glu Arg Asp Asp
 50 55 60
 Asp Val Pro Ala Asp Met Val Ala Glu Glu Ser Gly Pro Gly Ala Gln
 65 70 75 80
 Asn Ser Pro Tyr Gln Leu Arg Arg Lys Thr Leu Leu Pro Lys Arg Thr
 85 90 95
 Ala Cys Pro Thr Lys Asn Ser Met Glu Gly Ala Ser Thr Ser Thr Thr
 100 105 110
 Glu Asn Phe Gly His Arg Ala Lys Arg Ala Arg Val Ser Gly Lys Ser
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130 135 140
 Pro Asp Glu Val Val Leu Lys Ile Phe Ser Tyr Leu Leu Glu Gln Asp
 145 150 155 160
 Leu Cys Arg Ala Ala Cys Val Cys Lys Arg Phe Ser Glu Leu Ala Asn
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 Met Glu Ala Gly Gly Leu Pro Leu Glu Leu Trp Arg Met Ile Leu Ala
 20 25 30
 Tyr Leu His Leu Pro Asp Leu Gly Arg Cys Ser Leu Val Cys Arg Ala
 35 40 45
 Trp Tyr Glu Leu Ile Leu Ser Leu Asp Ser Thr Arg Trp Arg Gln Leu
 50 55 60
 Cys Leu Gly Cys Thr Glu Cys Arg His Pro Asn Trp Pro Asn Gln Pro
 65 70 75 80
 Asp Val Glu Pro Glu Ser Trp Arg Glu Ala Phe Lys Gln His Tyr Leu
 85 90 95
 Ala Ser Lys Thr Trp Thr Lys Asn Ala Leu Asp Leu Glu Ser Ser Ile
 100 105 110
 Cys Phe Ser Leu Phe Arg Arg Arg Arg Glu Arg Arg Thr Leu Ser Val
 115 120 125

Gly Pro Gly Arg Glu Phe Asp Ser Leu Gly Ser Ala Leu Ala Met Ala
 130 135 140

Ser Leu Tyr Asp Arg Ile Val Leu Phe Pro Gly Val Tyr Glu Glu Gln
 145 150 155 160

Gly Glu Ile Ile Leu Lys Val Pro Val Glu Ile Val Gly Gln Gly Lys
 165 170 175

Leu Gly

<210> 35
 <211> 751
 <212> DNA
 <213> Homo sapiens

<400> 35
 gagaccgaga cggcgccgct gaccctagag tcgctgccc aacgatcccct gctcctcatc 60
 ttatcctttt tggactatcg ggatctaata aactgttggt atgtcagtcg aagattaagc 120
 cagctatcaa gtcgatgatcc gctgtggaga agacattgca aaaaataactg gctgatatct 180
 gaggaagaga aaacacagaa gaatcagtgt tggaaatctc tcttcataga tacttactct 240
 gatgtaggaa gatacattga ccattatgct gctattaaaa aggctcggg aatgatctca 300
 agaaatattt ggagcccagg tgcctcggga tgggttttat ctctgaaaga ggggtgctcg 360
 agaggaagac ctcgatgctg tggaagcgca gattgggctg caagtttcct ggacgattat 420
 cgatgttcat accgaattca caatggacag aagttagttg gttcctgggg ttattgggaa 480
 gcatggcact gtctaatacac tatcgttctg aagatttggt agacgtcgat acagctgccg 540
 gagattccag cagagacagg gactgaaata ctgtctccct ttaacttttg catacatact 600
 ggtttgagtc agtacatagc agtggaagct gcagagggtt gaaacaaaaa tgaagttttc 660
 taccaatgtc agacagtaga acgtgtgttt aaatatggca ttaagatgtg ttctgatggg 720
 tgtataaatg gcatgcatta ggtattttca g 751

<210> 36
 <211> 247
 <212> PRT
 <213> Homo sapiens

<400> 36
 Glu Thr Glu Thr Ala Pro Leu Thr Leu Glu Ser Leu Pro Thr Asp Pro
 1 5 10 15
 Leu Leu Leu Ile Leu Ser Phe Leu Asp Tyr Arg Asp Leu Ile Asn Cys
 20 25 30
 Cys Tyr Val Ser Arg Arg Leu Ser Gln Leu Ser Ser His Asp Pro Leu
 35 40 45
 Trp Arg Arg His Cys Lys Lys Tyr Trp Leu Ile Ser Glu Glu Glu Lys
 50 55 60
 Thr Gln Lys Asn Gln Cys Trp Lys Ser Leu Phe Ile Asp Thr Tyr Ser
 65 70 75 80
 Asp Val Gly Arg Tyr Ile Asp His Tyr Ala Ala Ile Lys Lys Ala Ser
 85 90 95
 Gly Met Ile Ser Arg Asn Ile Trp Ser Pro Gly Val Leu Gly Trp Val
 100 105 110
 Leu Ser Leu Lys Glu Gly Cys Ser Arg Gly Arg Pro Arg Cys Cys Gly

115					120					125					
Ser	Ala	Asp	Trp	Ala	Ala	Ser	Phe	Leu	Asp	Asp	Tyr	Arg	Cys	Ser	Tyr
130					135					140					
Arg	Ile	His	Asn	Gly	Gln	Lys	Leu	Val	Gly	Ser	Trp	Gly	Tyr	Trp	Glu
145					150					155					160
Ala	Trp	His	Cys	Leu	Ile	Thr	Ile	Val	Leu	Lys	Ile	Cys	Thr	Ser	Ile
				165					170					175	
Gln	Leu	Pro	Glu	Ile	Pro	Ala	Glu	Thr	Gly	Thr	Glu	Ile	Leu	Ser	Pro
			180					185					190		
Phe	Asn	Phe	Cys	Ile	His	Thr	Gly	Leu	Ser	Gln	Tyr	Ile	Ala	Val	Glu
		195					200					205			
Ala	Ala	Glu	Gly	Asn	Lys	Asn	Glu	Val	Phe	Tyr	Gln	Cys	Gln	Thr	Val
	210					215					220				
Glu	Arg	Val	Phe	Lys	Tyr	Gly	Ile	Lys	Met	Cys	Ser	Asp	Gly	Cys	Ile
225				230						235					240
Asn	Gly	Met	His	Val	Phe	Ser									
				245											

<210> 37
 <211> 368
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> all n positions
 <223> n=a, c, g or t

<400> 37
 ggctccggtt tccggggccgg cgggtggccg ctcaccatgc ccgnaagca ccagcatttc 60
 caggaacctg aggtcggctg ctgcgggaaa tacttctgt ttggcttcaa cattgtcttc 120
 tgggtgctgg gagcctgtt cctggctatc ggcctctggg cctggggtga gaaggcggtt 180
 ctctcgaaca tctcagcgct gacagatctg ggaggccttg accccgtgtg gcttgtttgt 240
 ggtagtgtga ggcgatcatgt cgggtgctggg ctttgctggg ctgcaattgg ggccctccgg 300
 gagaacacct tctgctcaa gttttctcnc gngttcctcg gtctcatctt cttcctggag 360
 ctggcaac 368

<210> 38
 <211> 122
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> all Xaa positions
 <223> Xaa=unknown amino acid residue

<400> 38
 Gly Ser Gly Phe Arg Ala Gly Gly Trp Pro Leu Thr Met Pro Gly Lys
 1 5 10 15
 His Gln His Phe Gln Glu Pro Glu Val Gly Cys Cys Gly Lys Tyr Phe

20	25	30
Leu Phe Gly Phe Asn Ile Val Phe Trp Val Leu Gly Ala Leu Phe Leu		
35	40	45
Ala Ile Gly Leu Trp Ala Trp Gly Glu Lys Gly Val Leu Ser Asn Ile		
50	55	60
Ser Ala Leu Thr Asp Leu Gly Gly Leu Asp Pro Val Trp Leu Val Cys		
65	70	75
Gly Ser Trp Arg Arg His Val Gly Ala Gly Leu Cys Trp Ala Ala Ile		
	85	90
		95
Gly Ala Leu Arg Glu Asn Thr Phe Leu Leu Lys Phe Phe Xaa Xaa Phe		
100	105	110
Leu Gly Leu Ile Phe Phe Leu Glu Leu Ala		
115	120	

<210> 39
 <211> 774
 <212> DNA
 <213> Homo sapiens

<400> 39
 gcggcgccgcg ccgcccgcgta cctggacgag ctgcccgcgag cgctgctgct gcgcgtgctg 60
 gccgcactgc cggccgcgcga gctggtgcag gcctgcccgc tgggtgtgcct gcgctggaag 120
 gagctggttg acggcgcccc gctgtggtg ctcaagtgcc agcaggagg gctggtgccc 180
 gagggcgccg tggaggagga gcgcgaccac tggcagcagt tctacttcct gagcaagcgg 240
 cggcgcaacc ttctgcgtaa cccgtgtggg gaagaggact tgggaaggctg gtgtgacgtg 300
 gagcatggtg gggacggctg gaggggtggag gagctgcctg gagacagtgg ggtggagttc 360
 acccacgatg agagcgtcaa gaagtacttc gcctcctcct ttgagtgggtg tcgcaaagca 420
 caggtcattg acctgcaggc tgagggctac tgggaggagc tgctggacac gactcagccg 480
 gccatcgttg tgaaggactg gtactcgggc cgcagcgacg ctgggtgcct ctacgagctc 540
 accgttaagc tactgtccga gcacgagaac gtgctggctg agttcagcag cgggcagggtg 600
 gcagtgcgcc aagacagtga cggcgggggc tggatggaga tctcccacac cttcaccgac 660
 tacgggcccg gcgtccgctt cgtccgcttc gagcacgggg ggcaggggctc cgtctactgg 720
 aagggtcgtt tcggggcccc ggtgaccaac agcagcgtgt gggtagaacc ctga 774

<210> 40
 <211> 257
 <212> PRT
 <213> Homo sapiens

<400> 40
Ala Ala Ala Ala Ala Tyr Leu Asp Glu Leu Pro Glu Pro Leu Leu
1 5 10 15
Leu Arg Val Leu Ala Ala Leu Pro Ala Ala Glu Leu Val Gln Ala Cys
20 25 30
Arg Leu Val Cys Leu Arg Trp Lys Glu Leu Val Asp Gly Ala Pro Leu
35 40 45
Trp Leu Leu Lys Cys Gln Gln Glu Gly Leu Val Pro Glu Gly Gly Val
50 55 60
Glu Glu Glu Arg Asp His Trp Gln Gln Phe Tyr Phe Leu Ser Lys Arg
65 70 75 80

Arg Arg Asn Leu Leu Arg Asn Pro Cys Gly Glu Glu Asp Leu Glu Gly
 85 90 95
 Trp Cys Asp Val Glu His Gly Gly Asp Gly Trp Arg Val Glu Glu Leu
 100 105 110
 Pro Gly Asp Ser Gly Val Glu Phe Thr His Asp Glu Ser Val Lys Lys
 115 120 125
 Tyr Phe Ala Ser Ser Phe Glu Trp Cys Arg Lys Ala Gln Val Ile Asp
 130 135 140
 Leu Gln Ala Glu Gly Tyr Trp Glu Glu Leu Leu Asp Thr Thr Gln Pro
 145 150 155 160
 Ala Ile Val Val Lys Asp Trp Tyr Ser Gly Arg Ser Asp Ala Gly Cys
 165 170 175
 Leu Tyr Glu Leu Thr Val Lys Leu Leu Ser Glu His Glu Asn Val Leu
 180 185 190
 Ala Glu Phe Ser Ser Gly Gln Val Ala Val Pro Gln Asp Ser Asp Gly
 195 200 205
 Gly Gly Trp Met Glu Ile Ser His Thr Phe Thr Asp Tyr Gly Pro Gly
 210 215 220
 Val Arg Phe Val Arg Phe Glu His Gly Gly Gln Gly Ser Val Tyr Trp
 225 230 235 240
 Lys Gly Trp Phe Gly Ala Arg Val Thr Asn Ser Ser Val Trp Val Glu
 245 250 255
 Pro

<210> 41
 <211> 957
 <212> DNA
 <213> Homo sapiens

<400> 41
 atgggcgaga aggcgggtccc tttgctaagg aggaggcggg tgaagagaag ctgcccttct 60
 tgtggctcgg agcttggggt tgaagagaag agggggaaaag gaaatccgat ttccatccag 120
 ttgttcccc cagagctggt ggagcatatc atctcattcc tcccagtcag agaccttggt 180
 gccctcggcc agacctgccg ctacttccac gaagtgtgcg atggggaagg cgtgtggaga 240
 cgcatctgtc gcagactcag tccgcgcctc caagatcagg acacgaaggg cctgtatttc 300
 caggcatttg gaggccgccc ccgatgtctc agcaagagcg tggccccctt gctagcccac 360
 ggctaccgcc gcttcttgcc caccaaggat cacgtcttca ttcttgacta cgtggggacc 420
 ctcttcttcc tcaaaaatgc cctggtctcc accctcggcc agatgcagtg gaagcgggcc 480
 tgctcgtatg ttgtgttggt tcgtggagcc aaggattttg cctcggaccc aaggtgtgac 540
 acagtttacc gtaaatacct ctacgtcttg gccactcggg agccgcagga agtgggtgggt 600
 accaccagca gccgggcctg tgactgtgtt gaggtctatc tgcagtctag tgggcagcgg 660
 gtcttcaaga tgacattcca ccactcaatg accttcaagc agatcgtgct ggttggtcag 720
 gagaccagc gggctctact gctcctcaca gaggaaggaa agatctactc tttggtagtg 780
 aatgagaccc agcttgacca gccacgctcc tacacggttc agctggccct gaggaagggt 840
 tcccactacc tgctcacct gcgcgtggcc tgcattgactt ccaaccagag cagcaccctc 900
 tacgtcacag atcctattct gtgctcttgg ctacaaccac cttggcctgg tggatga 957

<210> 42
 <211> 318
 <212> PRT
 <213> Homo sapiens

<400> 42
 Met Gly Glu Lys Ala Val Pro Leu Leu Arg Arg Arg Arg Val Lys Arg
 1 5 10 15
 Ser Cys Pro Ser Cys Gly Ser Glu Leu Gly Val Glu Glu Lys Arg Gly
 20 25 30
 Lys Gly Asn Pro Ile Ser Ile Gln Leu Phe Pro Pro Glu Leu Val Glu
 35 40 45
 His Ile Ile Ser Phe Leu Pro Val Arg Asp Leu Val Ala Leu Gly Gln
 50 55 60
 Thr Cys Arg Tyr Phe His Glu Val Cys Asp Gly Glu Gly Val Trp Arg
 65 70 75 80
 Arg Ile Cys Arg Arg Leu Ser Pro Arg Leu Gln Asp Gln Asp Thr Lys
 85 90 95
 Gly Leu Tyr Phe Gln Ala Phe Gly Gly Arg Arg Arg Cys Leu Ser Lys
 100 105 110
 Ser Val Ala Pro Leu Leu Ala His Gly Tyr Arg Arg Phe Leu Pro Thr
 115 120 125
 Lys Asp His Val Phe Ile Leu Asp Tyr Val Gly Thr Leu Phe Phe Leu
 130 135 140
 Lys Asn Ala Leu Val Ser Thr Leu Gly Gln Met Gln Trp Lys Arg Ala
 145 150 155 160
 Cys Arg Tyr Val Val Leu Cys Arg Gly Ala Lys Asp Phe Ala Ser Asp
 165 170 175
 Pro Arg Cys Asp Thr Val Tyr Arg Lys Tyr Leu Tyr Val Leu Ala Thr
 180 185 190
 Arg Glu Pro Gln Glu Val Val Gly Thr Thr Ser Ser Arg Ala Cys Asp
 195 200 205
 Cys Val Glu Val Tyr Leu Gln Ser Ser Gly Gln Arg Val Phe Lys Met
 210 215 220
 Thr Phe His His Ser Met Thr Phe Lys Gln Ile Val Leu Val Gly Gln
 225 230 235 240
 Glu Thr Gln Arg Ala Leu Leu Leu Leu Thr Glu Glu Gly Lys Ile Tyr
 245 250 255
 Ser Leu Val Val Asn Glu Thr Gln Leu Asp Gln Pro Arg Ser Tyr Thr
 260 265 270
 Val Gln Leu Ala Leu Arg Lys Val Ser His Tyr Leu Pro His Leu Arg
 275 280 285

Val Ala Cys Met Thr Ser Asn Gln Ser Ser Thr Leu Tyr Val Thr Asp
 290 295 300

Pro Ile Leu Cys Ser Trp Leu Gln Pro Pro Trp Pro Gly Gly
 305 310 315

<210> 43
 <211> 1590
 <212> DNA
 <213> Homo sapiens

<400> 43
 cgagggggaa gcgaagggaag gggaagagga agggaaaagc gagcgagagg ggcaaggcgg 60
 aagaggaagc agggcggaag ggaagcccg gccgcagacg gcgaaggagg cagcggggccg 120
 ggggctgagg cgggagcgag gacacgccc aagagaggaag cagagggagg cggaagcgtg 180
 gaggaagggg cgagaggcat catcaaagga gatgagggga gcgtaggggc cgggaaagag 240
 gcacaaggaa gaaagtatgg gaaggaggaa tggaggggtca gggctaggcg gcgggagggc 300
 gccaggcccg gaagagtaca aggacaagga ggtcaggttt gggcctacat cccggggaca 360
 ggggcgggcca tggcgggcggc agccaggagg gaggaggagg aggcggctcg ggagtcagcc 420
 gcctgcccgg ctgcggggcc agcgctctgg cgcctggccc aagtgtctgt gctgcacatg 480
 tgctcttacc tcgacatgcg ggccctcggc cgcctggccc aggtgtaccg ctggctgtgg 540
 cacttcacca actgcgacct gctccggcgc cagatagcct gggcctcgtc caactccggc 600
 ttcacgcggc tcggcaccaa cctgatgacc agtgtcccag tgaagggtgtc tcagaactgg 660
 atagtggggg gctgcccaga ggggattctg ctgaagtggg gatgcagtca gatgccctgg 720
 atgcagctag aggatgatgc tttgtacata tcccaggcta atttcacatc gccctaccag 780
 ttccgtccag atggtgccag cttgaaccgt cagcctcttg gagtctctgc tgggcatgat 840
 gaggacgttt gccactttgt gctggccacc tcgcatattg tcagtgcagg aggagatggg 900
 aagattggcc ttggtaatat tcacagcacc ttcgctgcca agtactgggc tcatgaacag 960
 gaggtgaact gtgtggattg caaagggggc atcatatcat ttggctccag ggacaggacg 1020
 gccaaaggtgt ggccttttggc ctcaggccag ctggggcagt gtttatacac catccagact 1080
 gaagaccaa tctgggtctgt tgctatcagg ccattactca gctcttttgt gacagggacg 1140
 gcttgtttgt ggcactttct acccctgaaa atctgggacc tcaacagtgg gcagctgatg 1200
 acacacttgg acagagactt tcccccaagg gctgggggtgc tggatgtcat atatgagtc 1260
 ccttttcgac tgctctcctg tggctatgac acctatgttc gctactggga ctgccgcacc 1320
 agtgtccgga aatgtgtcat ggagtgggag gagccccaca acagcaccct gtactgcctg 1380
 cagacagatg gcaaccactt gcttgccaca ggttcctcct tctatagcgt tgtacggctg 1440
 tgggaccggc accaaagggc ctgcccgcac accttcccgc tgacgtcgac ccgcctcggc 1500
 agccctgtgt actgcctgca tctcaccacc aagcatctct atgctgcgct gtcttacaac 1560
 ctccacgtcc tggatattca aaaccctgta 1590

<210> 44
 <211> 529
 <212> PRT
 <213> Homo sapiens

<400> 44
 Arg Gly Gly Ser Glu Gly Arg Gly Arg Gly Arg Glu Lys Arg Ala Arg
 1 5 10 15
 Gly Ala Arg Arg Lys Arg Lys Gln Gly Gly Arg Glu Ala Arg Ala Ala
 20 25 30
 Asp Gly Glu Gly Gly Ser Gly Pro Gly Ala Glu Ala Gly Ala Arg Thr
 35 40 45
 Arg Pro Arg Glu Glu Ala Glu Gly Gly Gly Ser Val Glu Glu Gly Ala
 50 55 60
 Arg Gly Ile Ile Lys Gly Asp Glu Gly Ser Val Gly Ala Gly Lys Glu
 65 70 75 80

Ala	Gln	Gly	Arg	Lys	Tyr	Gly	Lys	Glu	Glu	Trp	Arg	Val	Arg	Ala	Arg	
				85					90					95		
Arg	Arg	Glu	Gly	Ala	Arg	Pro	Gly	Arg	Val	Gln	Gly	Gln	Gly	Gly	Gln	
			100					105					110			
Val	Trp	Ala	Tyr	Ile	Pro	Gly	Thr	Gly	Ala	Ala	Met	Ala	Ala	Ala	Ala	
		115					120					125				
Arg	Glu	Glu	Glu	Glu	Glu	Ala	Ala	Arg	Glu	Ser	Ala	Ala	Cys	Pro	Ala	
	130					135					140					
Ala	Gly	Pro	Ala	Leu	Trp	Arg	Leu	Pro	Glu	Val	Leu	Leu	Leu	His	Met	
145					150					155					160	
Cys	Ser	Tyr	Leu	Asp	Met	Arg	Ala	Leu	Gly	Arg	Leu	Ala	Gln	Val	Tyr	
			165						170					175		
Arg	Trp	Leu	Trp	His	Phe	Thr	Asn	Cys	Asp	Leu	Leu	Arg	Arg	Gln	Ile	
		180						185					190			
Ala	Trp	Ala	Ser	Leu	Asn	Ser	Gly	Phe	Thr	Arg	Leu	Gly	Thr	Asn	Leu	
	195						200					205				
Met	Thr	Ser	Val	Pro	Val	Lys	Val	Ser	Gln	Asn	Trp	Ile	Val	Gly	Cys	
	210					215					220					
Cys	Arg	Glu	Gly	Ile	Leu	Leu	Lys	Trp	Arg	Cys	Ser	Gln	Met	Pro	Trp	
225					230					235					240	
Met	Gln	Leu	Glu	Asp	Asp	Ala	Leu	Tyr	Ile	Ser	Gln	Ala	Asn	Phe	Ile	
			245						250					255		
Leu	Ala	Tyr	Gln	Phe	Arg	Pro	Asp	Gly	Ala	Ser	Leu	Asn	Arg	Gln	Pro	
		260						265					270			
Leu	Gly	Val	Ser	Ala	Gly	His	Asp	Glu	Asp	Val	Cys	His	Phe	Val	Leu	
	275						280					285				
Ala	Thr	Ser	His	Ile	Val	Ser	Ala	Gly	Gly	Asp	Gly	Lys	Ile	Gly	Leu	
	290					295					300					
Gly	Lys	Ile	His	Ser	Thr	Phe	Ala	Ala	Lys	Tyr	Trp	Ala	His	Glu	Gln	
305					310					315					320	
Glu	Val	Asn	Cys	Val	Asp	Cys	Lys	Gly	Gly	Ile	Ile	Ser	Phe	Gly	Ser	
			325						330					335		
Arg	Asp	Arg	Thr	Ala	Lys	Val	Trp	Pro	Leu	Ala	Ser	Gly	Gln	Leu	Gly	
			340					345					350			
Gln	Cys	Leu	Tyr	Thr	Ile	Gln	Thr	Glu	Asp	Gln	Ile	Trp	Ser	Val	Ala	
		355					360					365				
Ile	Arg	Pro	Leu	Leu	Ser	Ser	Phe	Val	Thr	Gly	Thr	Ala	Cys	Cys	Gly	
	370					375					380					
His	Phe	Ser	Pro	Leu	Lys	Ile	Trp	Asp	Leu	Asn	Ser	Gly	Gln	Leu	Met	
385					390					395					400	

Thr His Leu Asp Arg Asp Phe Pro Pro Arg Ala Gly Val Leu Asp Val
 405 410 415
 Ile Tyr Glu Ser Pro Phe Ala Leu Leu Ser Cys Gly Tyr Asp Thr Tyr
 420 425 430
 Val Arg Tyr Trp Asp Cys Arg Thr Ser Val Arg Lys Cys Val Met Glu
 435 440 445
 Trp Glu Glu Pro His Asn Ser Thr Leu Tyr Cys Leu Gln Thr Asp Gly
 450 455 460
 Asn His Leu Leu Ala Thr Gly Ser Ser Phe Tyr Ser Val Val Arg Leu
 465 470 475 480
 Trp Asp Arg His Gln Arg Ala Cys Pro His Thr Phe Pro Leu Thr Ser
 485 490 495
 Thr Arg Leu Gly Ser Pro Val Tyr Cys Leu His Leu Thr Thr Lys His
 500 505 510
 Leu Tyr Ala Ala Leu Ser Tyr Asn Leu His Val Leu Asp Ile Gln Asn
 515 520 525

Pro

<210> 45
 <211> 1214
 <212> DNA
 <213> Homo sapiens

<400> 45
 gcattgctat aatttttacta tactctcatc taaatctaaa atcagtcttc aaaataaaaa 60
 caaattgtcc ttgccaataa atttttttaa tcgcacaatt aattgacatt aactgccaat 120
 tctttttggc taattgacta attttaactt ctgtgttgct tttccagagg catggctatt 180
 gcaccttggg agaagccttt aatcggttag acttctcaag tgcaattcaa gatatccgaa 240
 cgttcaatta tgtggtcaaa ctgttgcagc taattgcaaa atcccagtta acttcattga 300
 gtggcgtggc acagaagaat tacttcaaca ttttggataa aatcgttcaa aaggttcttg 360
 atgaccacca caatcctcgc ttaatcaaag atcttctgca agacctaaag tctaccctct 420
 gcattcttat tagaggagta gggaagtctg tattagtggg aaacatcaat atttggattt 480
 gccgattaga aactattctc gcctggcaac aacagctaca ggatcttcag atgactaagc 540
 aagtgaacaa tggcctcacc ctcaagtacc ttcctctgca catgctgaac aacatcctat 600
 accggttctc agacggatgg gacatcatca ccttaggcca ggtgaccccc acgttgtata 660
 tgcttagtga agacagacag ctgtggaaga agctttgtca gtaccatttt gctgaaaagc 720
 agttttgtag acatttgatc ctttcagaaa aagggtcatat tgaatggaag ttgatgtact 780
 ttgcacttca gaaacattac ccagcgaagg agcagtagcg agacacactg catttctgtc 840
 ggcactgcag cattctcttt tggaaggact caggacaccc ctgcacggcg gccgaccctg 900
 acagctgctt cacgcctgtg tctccgcagc acttcacga cctcttcaag ttttaagggc 960
 tgccctgcc atccctattg gagattgtga atcctgctgt ctgtgcaggg ctcatagtga 1020
 gtgttctgtg aggtgggtgg agactcctcg gaagccctg cttccagaaa gcctgggaag 1080
 aactgccctt ctgcaaaggg gggactgcat ggttgcattt tcatcactga aagtcagagg 1140

 ccaaggaaat catttctact tctttaaaaa ctccttctaa gcatattaaa atgtgaaatt 1200
 ttgcgtactc tctc 1214

<210> 46
 <211> 272
 <212> PRT
 <213> Homo sapiens

<400> 46

Leu	Ile	Leu	Thr	Ser	Val	Leu	Leu	Phe	Gln	Arg	His	Gly	Tyr	Cys	Thr
1				5					10					15	
Leu	Gly	Glu	Ala	Phe	Asn	Arg	Leu	Asp	Phe	Ser	Ser	Ala	Ile	Gln	Asp
			20					25					30		
Ile	Arg	Thr	Phe	Asn	Tyr	Val	Val	Lys	Leu	Leu	Gln	Leu	Ile	Ala	Lys
		35					40					45			
Ser	Gln	Leu	Thr	Ser	Leu	Ser	Gly	Val	Ala	Gln	Lys	Asn	Tyr	Phe	Asn
	50					55					60				
Ile	Leu	Asp	Lys	Ile	Val	Gln	Lys	Val	Leu	Asp	Asp	His	His	Asn	Pro
65					70					75					80
Arg	Leu	Ile	Lys	Asp	Leu	Leu	Gln	Asp	Leu	Ser	Ser	Thr	Leu	Cys	Ile
				85					90					95	
Leu	Ile	Arg	Gly	Val	Gly	Lys	Ser	Val	Leu	Val	Gly	Asn	Ile	Asn	Ile
			100					105					110		
Trp	Ile	Cys	Arg	Leu	Glu	Thr	Ile	Leu	Ala	Trp	Gln	Gln	Gln	Leu	Gln
		115					120					125			
Asp	Leu	Gln	Met	Thr	Lys	Gln	Val	Asn	Asn	Gly	Leu	Thr	Leu	Ser	Asp
	130					135					140				
Leu	Pro	Leu	His	Met	Leu	Asn	Asn	Ile	Leu	Tyr	Arg	Phe	Ser	Asp	Gly
145					150					155					160
Trp	Asp	Ile	Ile	Thr	Leu	Gly	Gln	Val	Thr	Pro	Thr	Leu	Tyr	Met	Leu
				165					170					175	
Ser	Glu	Asp	Arg	Gln	Leu	Trp	Lys	Lys	Leu	Cys	Gln	Tyr	His	Phe	Ala
			180					185					190		
Glu	Lys	Gln	Phe	Cys	Arg	His	Leu	Ile	Leu	Ser	Glu	Lys	Gly	His	Ile
		195					200					205			
Glu	Trp	Lys	Leu	Met	Tyr	Phe	Ala	Leu	Gln	Lys	His	Tyr	Pro	Ala	Lys
	210					215					220				
Glu	Gln	Tyr	Gly	Asp	Thr	Leu	His	Phe	Cys	Arg	His	Cys	Ser	Ile	Leu
225					230					235					240
Phe	Trp	Lys	Asp	Ser	Gly	His	Pro	Cys	Thr	Ala	Ala	Asp	Pro	Asp	Ser
				245					250					255	
Cys	Phe	Thr	Pro	Val	Ser	Pro	Gln	His	Phe	Ile	Asp	Leu	Phe	Lys	Phe
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<210> 47
 <211> 4059
 <212> DNA

<213> Homo sapiens

<400> 47

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tgcgcacact	gagcacgccc	agcccagccc	tgatatgtcc	accgaatctc	ccaggatttc	180
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ctcctactgt	aggctcctgt	gcatactgtc	gtcttctgtg	ggggatggag	aggttagtgt	3360
gatgagggtg	tgtctgcccc	ggagggtttct	ttcaaacatc	atggcctccc	atccaatcaa	3420

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catcatcaaa ttacatgtgt aatcaaggct ctgtgccatg ggggaaatga atcatttagc 3480
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<210> 48
 <211> 483
 <212> PRT
 <213> Homo sapiens

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<400> 48
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Ser Ser Thr Asp His Thr Pro Thr Lys Ala Gln Lys Asn Val Ala Thr
      20              25              30

Ser Glu Asp Ser Asp Leu Ser Met Arg Thr Leu Ser Thr Pro Ser Pro
      35              40              45

Ala Leu Ile Cys Pro Pro Asn Leu Pro Gly Phe Gln Asn Gly Arg Gly
      50              55              60

Ser Ser Thr Ser Ser Ser Ser Ile Thr Gly Glu Thr Val Ala Met Val
      65              70              75              80

His Ser Pro Pro Pro Thr Arg Leu Thr His Pro Leu Ile Arg Leu Ala
      85              90              95

Ser Arg Pro Gln Lys Glu Gln Ala Ser Ile Asp Arg Leu Pro Asp His
      100              105              110

Ser Met Val Gln Ile Phe Ser Phe Leu Pro Thr Asn Gln Leu Cys Arg
      115              120              125

Cys Ala Arg Val Cys Arg Arg Trp Tyr Asn Leu Ala Trp Asp Pro Arg
      130              135              140

Leu Trp Arg Thr Ile Arg Leu Thr Gly Glu Thr Ile Asn Val Asp Arg
      145              150              155              160

Ala Leu Lys Val Leu Thr Arg Arg Leu Cys Gln Asp Thr Pro Asn Val
      165              170              175

Cys Leu Met Leu Glu Thr Val Thr Val Ser Gly Cys Arg Arg Leu Thr
      180              185              190

Asp Arg Gly Leu Tyr Thr Ile Ala Gln Cys Cys Pro Glu Leu Arg Arg
      195              200              205

Leu Glu Val Ser Gly Cys Tyr Asn Ile Ser Asn Glu Ala Val Phe Asp
      210              215              220

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Val Val Ser Leu Cys Pro Asn Leu Glu His Leu Asp Val Ser Gly Cys
 225 230 235 240
 Ser Lys Val Thr Cys Ile Ser Leu Thr Arg Glu Ala Ser Ile Lys Leu
 245 250 255
 Ser Pro Leu His Gly Lys Gln Ile Ser Ile Arg Tyr Leu Asp Met Thr
 260 265 270
 Asp Cys Phe Val Leu Glu Asp Glu Gly Leu His Thr Ile Ala Ala His
 275 280 285
 Cys Thr Gln Leu Thr His Leu Tyr Leu Arg Arg Cys Val Arg Leu Thr
 290 295 300
 Asp Glu Gly Leu Arg Tyr Leu Val Ile Tyr Cys Ala Ser Ile Lys Glu
 305 310 315 320
 Leu Ser Val Ser Asp Cys Arg Phe Val Ser Asp Phe Gly Leu Arg Glu
 325 330 335
 Ile Ala Lys Leu Glu Ser Arg Leu Arg Tyr Leu Ser Ile Ala His Cys
 340 345 350
 Gly Arg Val Thr Asp Val Gly Ile Arg Tyr Val Ala Lys Tyr Cys Ser
 355 360 365
 Lys Leu Arg Tyr Leu Asn Ala Arg Gly Cys Glu Gly Ile Thr Asp His
 370 375 380
 Gly Val Glu Tyr Leu Ala Lys Asn Cys Thr Lys Leu Lys Ser Leu Asp
 385 390 395 400
 Ile Gly Lys Cys Pro Leu Val Ser Asp Thr Gly Leu Glu Cys Leu Ala
 405 410 415
 Leu Asn Cys Phe Asn Leu Lys Arg Leu Ser Leu Lys Ser Cys Glu Ser
 420 425 430
 Ile Thr Gly Gln Gly Leu Gln Ile Val Ala Ala Asn Cys Phe Asp Leu
 435 440 445
 Gln Thr Leu Asn Val Gln Asp Cys Glu Val Ser Val Glu Ala Leu Arg
 450 455 460
 Phe Val Lys Arg His Cys Lys Arg Cys Val Ile Glu His Thr Asn Pro
 465 470 475 480
 Ala Phe Phe

<210> 49
 <211> 850
 <212> DNA
 <213> Homo sapiens

<400> 49
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 gggctgggga gaccgcattc ccttggaat cctggtgcag attttcgggt tgttggtggc 120
 ggcggacggc cccatgccct tctgggcag ggctgcgcgc gtgtgccgcc gctggcagga 180


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ggccgcttcc caaccgcgc tctggcacac cgtgaccctg tcgtccccgc tggtcggccg 240
gcctgccaag ggcggggtca aggcggagaa gaagctcctt gcttccctgg agtggcttat 300
gccaatcgg ttttcacagc tccagaggct gacctcatc cactggaagt ctcaggtaca 360
ccccgtgttg aagctggtag gtgagtgtg tctcgggtc actttcctca agctctccgg 420
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caaccgtaat agcattcccc ttcagctgcc tgtcgaggct ctgcagaaaag gctgccctca 720
gctccagggt ctgcggctgt tgaacctgat gtggctgccc aagcctccgg gacgaggggt 780
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<210> 50
 <211> 283
 <212> PRT
 <213> Homo sapiens

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<400> 50
Ala Ala Ala Pro Ala Pro Ala Pro Ala Pro Thr Pro Thr Pro Glu Glu
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Gly Pro Asp Ala Gly Trp Gly Asp Arg Ile Pro Leu Glu Ile Leu Val
      20              25              30

Gln Ile Phe Gly Leu Leu Val Ala Ala Asp Gly Pro Met Pro Phe Leu
      35              40              45

Gly Arg Ala Ala Arg Val Cys Arg Arg Trp Gln Glu Ala Ala Ser Gln
      50              55              60

Pro Ala Leu Trp His Thr Val Thr Leu Ser Ser Pro Leu Val Gly Arg
      65              70              75              80

Pro Ala Lys Gly Gly Val Lys Ala Glu Lys Lys Leu Leu Ala Ser Leu
      85              90              95

Glu Trp Leu Met Pro Asn Arg Phe Ser Gln Leu Gln Arg Leu Thr Leu
      100              105              110

Ile His Trp Lys Ser Gln Val His Pro Val Leu Lys Leu Val Gly Glu
      115              120              125

Cys Cys Pro Arg Leu Thr Phe Leu Lys Leu Ser Gly Cys His Gly Val
      130              135              140

Thr Ala Asp Ala Leu Val Met Leu Ala Lys Ala Cys Cys Gln Leu His
      145              150              155              160

Ser Leu Asp Leu Gln His Ser Met Val Glu Ser Thr Ala Val Val Ser
      165              170              175

Phe Leu Glu Glu Ala Gly Ser Arg Met Arg Lys Leu Trp Leu Thr Tyr
      180              185              190

Ser Ser Gln Thr Thr Ala Ile Leu Gly Ala Leu Leu Gly Ser Cys Cys
      195              200              205

Pro Gln Leu Gln Val Leu Glu Val Ser Thr Gly Ile Asn Arg Asn Ser
      210              215              220

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Ile Pro Leu Gln Leu Pro Val Glu Ala Leu Gln Lys Gly Cys Pro Gln
 225 230 235 240

Leu Gln Val Leu Arg Leu Leu Asn Leu Met Trp Leu Pro Lys Pro Pro
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Gly Arg Gly Val Ala Pro Gly Pro Gly Phe Pro Ser Leu Glu Glu Leu
 260 265 270

Cys Leu Ala Ser Ser Thr Cys Asn Phe Val Ser
 275 280

<210> 51
 <211> 1777
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> all n positions
 <223> n=a, c, g or t

<400> 51
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 agaagtgtca gaacactcca caggtataac ccatcttcct cctgaggtaa tgctgtcaat 180
 tttcagctat cttaatcctc aagagttatg tcgatgcagt caagtaagca tgaaatgggtc 240
 tcagctgaca aaaacgggat cgctttggaa acatctttac cctgttcatt gggccagagg 300
 tgactggat agtgggtccc caactgaact tgatactgaa cctgatgatg aatgggtgaa 360
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 tgatctttgt ctacttcatt tagctgagca ggctttcttt catgcacttt actcatagca 1680
 catttcttgt gttaaccatc cttttttgag cgtgacttgt tttgggcccc ttnyttacaa 1740
 cttcagaaat cttaattacc agtgrattgt aatgttg 1777

<210> 52
 <211> 590
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> all Xaa positions
 <223> Xaa=unknown amino acid residue

 <400> 52
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 Leu Trp Asn His Ala Glu Glu Arg Gln Lys Phe Phe Lys Tyr Ser Val
 20 25 30
 Asp Glu Lys Ser Asp Lys Glu Ala Glu Val Ser Glu His Ser Thr Gly
 35 40 45
 Ile Thr His Leu Pro Pro Glu Val Met Leu Ser Ile Phe Ser Tyr Leu
 50 55 60
 Asn Pro Gln Glu Leu Cys Arg Cys Ser Gln Val Ser Met Lys Trp Ser
 65 70 75 80
 Gln Leu Thr Lys Thr Gly Ser Leu Trp Lys His Leu Tyr Pro Val His
 85 90 95
 Trp Ala Arg Gly Asp Trp Tyr Ser Gly Pro Ala Thr Glu Leu Asp Thr
 100 105 110
 Glu Pro Asp Asp Glu Trp Val Lys Asn Arg Lys Asp Glu Ser Arg Ala
 115 120 125
 Phe His Glu Trp Asp Glu Asp Ala Asp Ile Asp Glu Ser Glu Glu Ser
 130 135 140
 Ala Glu Glu Ser Ile Ala Ile Ser Ile Ala Gln Met Glu Lys Arg Leu
 145 150 155 160
 Leu His Gly Leu Ile His Asn Val Leu Pro Tyr Val Gly Thr Ser Val
 165 170 175

 Lys Thr Leu Val Leu Ala Tyr Ser Ser Ala Val Ser Ser Lys Met Val
 180 185 190
 Arg Gln Ile Leu Glu Leu Cys Pro Asn Leu Glu His Leu Asp Leu Thr
 195 200 205

 Gln Thr Asp Ile Ser Asp Ser Ala Phe Asp Ser Trp Ser Trp Leu Gly
 210 215 220
 Cys Cys Gln Ser Leu Arg His Leu Asp Leu Ser Gly Cys Glu Lys Ile
 225 230 235 240
 Thr Asp Val Ala Leu Glu Lys Ile Ser Arg Ala Leu Gly Ile Leu Thr
 245 250 255
 Ser His Gln Ser Gly Phe Leu Lys Thr Ser Thr Ser Lys Ile Thr Ser
 260 265 270
 Thr Ala Trp Lys Asn Lys Asp Ile Thr Met Gln Ser Thr Lys Gln Tyr
 275 280 285

Ala	Cys	Leu	His	Asp	Leu	Thr	Asn	Lys	Gly	Ile	Gly	Glu	Glu	Ile	Asp	290	295	300
Asn	Glu	His	Pro	Trp	Thr	Lys	Pro	Val	Ser	Ser	Glu	Asn	Phe	Thr	Ser	305	310	315
Pro	Tyr	Val	Trp	Met	Leu	Asp	Ala	Glu	Asp	Leu	Ala	Asp	Ile	Glu	Asp	325	330	335
Thr	Val	Glu	Trp	Arg	His	Arg	Asn	Val	Glu	Ser	Leu	Cys	Val	Met	Glu	340	345	350
Thr	Ala	Ser	Asn	Phe	Ser	Cys	Ser	Thr	Ser	Gly	Cys	Phe	Ser	Lys	Asp	355	360	365
Ile	Val	Gly	Leu	Arg	Thr	Ser	Val	Cys	Trp	Gln	Gln	His	Cys	Ala	Ser	370	375	380
Pro	Ala	Phe	Ala	Tyr	Cys	Gly	His	Ser	Phe	Cys	Cys	Thr	Gly	Thr	Ala	385	390	395
Leu	Arg	Thr	Met	Ser	Ser	Leu	Pro	Glu	Ser	Ser	Ala	Met	Cys	Arg	Lys	405	410	415
Ala	Ala	Arg	Thr	Arg	Leu	Pro	Arg	Gly	Lys	Asp	Leu	Ile	Tyr	Phe	Gly	420	425	430
Ser	Glu	Lys	Ser	Asp	Gln	Glu	Thr	Gly	Arg	Val	Leu	Leu	Phe	Leu	Ser	435	440	445
Leu	Ser	Gly	Cys	Tyr	Gln	Ile	Thr	Asp	His	Gly	Leu	Arg	Val	Leu	Thr	450	455	460
Leu	Gly	Gly	Gly	Leu	Pro	Tyr	Leu	Glu	His	Leu	Asn	Leu	Ser	Gly	Cys	465	470	475
Leu	Thr	Ile	Thr	Gly	Ala	Gly	Leu	Gln	Asp	Leu	Val	Ser	Ala	Cys	Pro	485	490	495
Ser	Leu	Asn	Asp	Glu	Tyr	Phe	Tyr	Tyr	Cys	Asp	Asn	Ile	Asn	Gly	Pro	500	505	510
His	Ala	Asp	Thr	Ala	Ser	Gly	Cys	Gln	Asn	Leu	Gln	Cys	Gly	Phe	Arg	515	520	525
Ala	Cys	Cys	Arg	Ser	Gly	Glu	Pro	Leu	Thr	Ser	Asp	Leu	Cys	Leu	Leu	530	535	540
His	Leu	Ala	Glu	Gln	Ala	Phe	Phe	His	Ala	Leu	Tyr	Ser	His	Ile	Ser	545	550	555
Cys	Val	Asn	His	Pro	Phe	Leu	Ser	Val	Thr	Cys	Phe	Gly	Pro	Ile	Xaa	565	570	575
Tyr	Asn	Phe	Arg	Asn	Leu	Asn	Tyr	Gln	Xaa	Ile	Val	Met	Leu			580	585	590

<210> 53
 <211> 1681
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> all n positions
 <223> n=a, c, g or t

<400> 53
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 gagggcaaaa ggagcactag ctaggtcaga gccatgtttc aggtcacaat gtgatgtcag 180
 atgttgctta taaatccttt cttgtcttcg ccattcttaa atcttgatag gtgcctgttg 240
 ggaaactgta aatgcctttc ccaatggaga atcaacagat tgggtgatgg tggagtcggt 300
 caggaagact caggtcttct agaggaaagg atgcctcatc accccttngg cccaggcagc 360
 tgctgtcaga gaatgacaca gcacctgcac agtcgctgtc cacttcctgc cactgctgtc 420
 ggtggggtga cgggagcaaa gtaggcgtgg actttgacat gagggagctg agcccgcatc 480
 cgcttgatgc ctgcacgggt aacctgctgg cagtcgtaca gctcgaggcg ctccaggcct 540
 cggcagttct ctagggtgtc cagggccaca tcagtgatga ggaggcagtt gtccaactcc 600
 agtaccgcga gcctctcatg gccacaggta ctggtgctca ggtgcaggat cccatcatct 660
 gkgatgagtt cacagtggga caggctcagg gcttgagtt taggacagtg aatggagagc 720
 tggatgagtg tgctgtcggg tatcaggatg cawtcttcaa gatccatctt ctccaattcg 780
 tggcaattcc gagctaaaag tgtaaaacct gcgtcagtc aatgggagca tcgggcagcc 840
 tccaaaattt gcagtcgcgg acagttcaaa cccagggtcg taagagaggc atctgtgagg 900
 ttgctgcaac ccgaaaggca gagagcctgt agccggtgac agcccctgca tatctgcacc 960
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 taattctgaa tgtgtttcag agcttcatct tctaactgtg tgcagcccct caggagcagg 1080
 gctttcaggc ctgcacaacc tcgcaccagt gcctcgatgc catccttcgt gatctgatca 1140
 caccaagaga ggttcaggta ctccaggttt cggcagccct cactgatccc cttcaaggag 1200
 ctggttgtaa tagacacaca ggaggtcaga wccagatggt tcagcttgga acagaatctg 1260
 ctaaggctat aacacgtgct gtcagtgatt tttgtgcac cattgagggt caaatgttca 1320
 atgtttcggc agttctgtgc aaaggtcttc aaggaggaat cccaacacc aatgcagcct 1380
 cgcaagctga gcttcctcag gaatccaacg catcgcttcg agatattttc caccactcga 1440
 ccctctacat ctatttgaaa gttaaaaaga tctattcttt gccagttgct tccatccagg 1500
 gctaagatgt tccaagcctt ggaaatctgt gcacatcggc acaaagttac tatatccaag 1560
 aagggaaata ttcttaacag aagttctttg ggtaactttt tgtaataaag gccttcatca 1620
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 c 1681

<210> 54
 <211> 437
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> all Xaa positions
 <223> Xaa=unknown amino acid residue

<400> 54
 Arg Val Thr Ser Gly Cys Gly Leu Ala Arg Gly Ser Ser Ala Met Val
 1 5 10 15
 Phe Ser Asn Asn Asp Glu Gly Leu Ile Asn Lys Lys Leu Pro Lys Glu
 20 25 30
 Leu Leu Leu Arg Ile Phe Ser Phe Leu Asp Ile Val Thr Leu Cys Arg
 35 40 45

Cys	Ala	Gln	Ile	Ser	Lys	Ala	Trp	Asn	Ile	Leu	Ala	Leu	Asp	Gly	Ser		
	50					55					60						
Asn	Trp	Gln	Arg	Ile	Asp	Leu	Phe	Asn	Phe	Gln	Ile	Asp	Val	Glu	Gly		
	65				70					75					80		
Arg	Val	Val	Glu	Asn	Ile	Ser	Lys	Arg	Cys	Val	Gly	Phe	Leu	Arg	Lys		
				85					90					95			
Leu	Ser	Leu	Arg	Gly	Cys	Ile	Gly	Val	Gly	Asp	Ser	Ser	Leu	Lys	Thr		
			100					105					110				
Phe	Ala	Gln	Asn	Cys	Arg	Asn	Ile	Glu	His	Leu	Asn	Leu	Asn	Gly	Cys		
		115					120					125					
Thr	Lys	Ile	Thr	Asp	Ser	Thr	Cys	Tyr	Ser	Leu	Ser	Arg	Phe	Cys	Ser		
	130					135					140						
Lys	Leu	Lys	His	Leu	Xaa	Leu	Thr	Ser	Cys	Val	Ser	Ile	Thr	Asn	Ser		
	145				150					155				160			
Ser	Leu	Lys	Gly	Ile	Ser	Glu	Gly	Cys	Arg	Asn	Leu	Glu	Tyr	Leu	Asn		
				165					170					175			
Leu	Ser	Trp	Cys	Asp	Gln	Ile	Thr	Lys	Asp	Gly	Ile	Glu	Ala	Leu	Val		
			180					185					190				
Arg	Gly	Cys	Arg	Gly	Leu	Lys	Ala	Leu	Leu	Leu	Arg	Gly	Cys	Thr	Gln		
		195					200					205					
Leu	Glu	Asp	Glu	Ala	Leu	Lys	His	Ile	Gln	Asn	Tyr	Cys	His	Glu	Leu		
	210					215					220						
Val	Ser	Leu	Asn	Leu	Gln	Ser	Cys	Ser	Arg	Ile	Thr	Asp	Glu	Gly	Val		
	225				230					235					240		
Val	Gln	Ile	Cys	Arg	Gly	Cys	His	Arg	Leu	Gln	Ala	Leu	Cys	Leu	Ser		
				245					250					255			
Gly	Cys	Ser	Asn	Leu	Thr	Asp	Ala	Ser	Leu	Thr	Ala	Leu	Gly	Leu	Asn		
			260					265					270				
Cys	Pro	Arg	Leu	Gln	Ile	Leu	Glu	Ala	Ala	Arg	Cys	Ser	His	Leu	Thr		
		275					280					285					
Asp	Ala	Gly	Phe	Thr	Leu	Leu	Ala	Arg	Asn	Cys	His	Glu	Leu	Glu	Lys		
	290					295					300						
Met	Asp	Leu	Glu	Xaa	Cys	Ile	Leu	Ile	Thr	Asp	Ser	Thr	Leu	Ile	Gln		
	305				310					315					320		
Leu	Ser	Ile	His	Cys	Pro	Lys	Leu	Gln	Ala	Leu	Ser	Leu	Ser	His	Cys		
				325					330					335			
Glu	Leu	Ile	Xaa	Asp	Asp	Gly	Ile	Leu	His	Leu	Ser	Asn	Ser	Thr	Cys		
			340				345						350				
Gly	His	Glu	Arg	Leu	Arg	Val	Leu	Glu	Leu	Asp	Asn	Cys	Leu	Leu	Ile		
		355					360					365					
Thr	Asp	Val	Ala	Leu	Xaa	His	Leu	Glu	Asn	Cys	Arg	Gly	Leu	Glu	Arg		

370	375	380
Leu Glu Leu Tyr Asp Cys Gln Gln Val Thr Arg Ala Gly Ile Lys Arg		
385	390	395 400
Met Arg Ala Gln Leu Pro His Val Lys Val His Ala Tyr Phe Ala Pro		
	405	410 415
Val Thr Pro Pro Thr Ala Val Ala Gly Ser Gly Gln Arg Leu Cys Arg		
	420	425 430
Cys Cys Val Ile Leu		
	435	

<210> 55
 <211> 1866
 <212> DNA
 <213> Homo sapiens

<400> 55

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cgccgagcca	ggacagctac	aagaggagaa	atgatgaaca	cccatagagc	tatagaatca	120
aacagccaga	cttcccctct	caatgcagag	gtagtccagt	atgccaaaga	agtagtggt	180
ttcagttccc	attatggaag	tgagaatagt	atgtcctata	ctatgtggaa	tttggctggt	240
gtaccaaag	tattcccaag	ttctggtgac	tttactcaga	cagctgtggt	tcgaacttat	300
gggacatggt	gggatcagtg	tcctagtgt	tccttgccat	tcaagaggac	gccaccta	360
tttcagagcc	aggactatgt	ggaacttact	tttgaacaac	aggtgtatcc	tacagctgta	420
catgtttctag	aaacctatca	tcccggagca	gtcattagaa	ttctcgcttg	ttctgcaaat	480
ccttattccc	caaattccacc	agctgaagta	agatgggaga	ttctttggtc	agagagacct	540
accgaagtg	atgtctccca	agctcgccag	tttaaaccct	gtattaagca	gataaatttc	600
cccacaaatc	ttatacgact	ggaagtaaat	agttctcttc	tgggaatatta	cactgaatta	660
gatgcagttg	tgctacatgg	tgtgaaggac	aagccagtgc	tttctctcaa	gacttcactt	720
attgacatga	atgatataga	agatgatgcc	tatgcagaaa	aggatggttg	tggaaatggac	780
agtcttaaca	aaaagttag	cagtgtgtgc	ctcggggaag	ggccaaataa	tgggtatttt	840
gataaactac	cttatgagct	tattcagctg	attctgaatc	atcttacact	accagacctg	900
tgtagattag	cacagacttg	caaactactg	agccagcatt	gctgtgatcc	tctgcaatac	960
atccacctca	atctgcaacc	atactgggca	aaactagatg	acacttctct	ggaatttcta	1020
cagtctcgct	gcactcttgt	ccagtggcct	aatttatctt	ggactggcaa	tagaggcttc	1080
atctctgttg	caggatttag	caggtttctg	aaggtttgtg	gatccgaatt	agtacgcctt	1140
gaattgtctt	gcagccactt	tcttaatgaa	acttgcttag	aagttatttc	tgagatgtgt	1200
ccaaatctac	aggccttaaa	tctctctctc	tgtgataagc	taccacctca	agctttcaac	1260
cacattgcca	agttatgcag	ccttaaacga	cttggtctct	atcgaacaaa	agtagagcaa	1320
acagcactgc	tcagcatgtt	gaacttctgt	tcagagcttc	agcacctcag	tttaggcagt	1380
tgtgtcatga	ttgaagacta	tgatgtgata	gctagcatga	taggagccaa	gtgtaaaaaa	1440
ctccggaccc	tggatctgtg	gagatgtaag	aatattactg	agaatggaat	agcagaactg	1500
gcttctgggt	gtccactact	ggaggagcct	gaccttggt	ggtgccccac	tctgcagagc	1560
agcaccgggt	gcttcaccag	actggcacac	cagctcccaa	acttgcaaaa	actctttctt	1620
acagctaata	gatctgtgtg	tgacacagac	attgatgaat	tggcatgtaa	ttgtaccagg	1680
ttacagcagc	tggacataat	aggaacaaga	atggtaagtc	cggcatcctt	aagaaaactc	1740
ctggaatctt	gtaaagatct	ttctttactt	gatgtgtcct	tctgttcgca	gattgataac	1800
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cagtga						1866

<210> 56
 <211> 621
 <212> PRT
 <213> Homo sapiens

<400> 56

Met Ser Pro Val Phe Pro Met Leu Thr Val Leu Thr Met Phe Tyr Tyr

1	5	10	15
Ile Cys Leu Arg Arg Arg Ala Arg Thr Ala Thr Arg Gly Glu Met Met	20	25	30
Asn Thr His Arg Ala Ile Glu Ser Asn Ser Gln Thr Ser Pro Leu Asn	35	40	45
Ala Glu Val Val Gln Tyr Ala Lys Glu Val Val Asp Phe Ser Ser His	50	55	60
Tyr Gly Ser Glu Asn Ser Met Ser Tyr Thr Met Trp Asn Leu Ala Gly	65	70	75
Val Pro Asn Val Phe Pro Ser Ser Gly Asp Phe Thr Gln Thr Ala Val	85	90	95
Phe Arg Thr Tyr Gly Thr Trp Trp Asp Gln Cys Pro Ser Ala Ser Leu	100	105	110
Pro Phe Lys Arg Thr Pro Pro Asn Phe Gln Ser Gln Asp Tyr Val Glu	115	120	125
Leu Thr Phe Glu Gln Gln Val Tyr Pro Thr Ala Val His Val Leu Glu	130	135	140
Thr Tyr His Pro Gly Ala Val Ile Arg Ile Leu Ala Cys Ser Ala Asn	145	150	155
Pro Tyr Ser Pro Asn Pro Pro Ala Glu Val Arg Trp Glu Ile Leu Trp	165	170	175
Ser Glu Arg Pro Thr Lys Val Asn Ala Ser Gln Ala Arg Gln Phe Lys	180	185	190
Pro Cys Ile Lys Gln Ile Asn Phe Pro Thr Asn Leu Ile Arg Leu Glu	195	200	205
Val Asn Ser Ser Leu Leu Glu Tyr Tyr Thr Glu Leu Asp Ala Val Val	210	215	220
Leu His Gly Val Lys Asp Lys Pro Val Leu Ser Leu Lys Thr Ser Leu	225	230	235
Ile Asp Met Asn Asp Ile Glu Asp Asp Ala Tyr Ala Glu Lys Asp Gly	245	250	255
Cys Gly Met Asp Ser Leu Asn Lys Lys Phe Ser Ser Ala Val Leu Gly	260	265	270
Glu Gly Pro Asn Asn Gly Tyr Phe Asp Lys Leu Pro Tyr Glu Leu Ile	275	280	285
Gln Leu Ile Leu Asn His Leu Thr Leu Pro Asp Leu Cys Arg Leu Ala	290	295	300
Gln Thr Cys Lys Leu Leu Ser Gln His Cys Cys Asp Pro Leu Gln Tyr	305	310	315
Ile His Leu Asn Leu Gln Pro Tyr Trp Ala Lys Leu Asp Asp Thr Ser	325	330	335

Leu Glu Phe Leu Gln Ser Arg Cys Thr Leu Val Gln Trp Leu Asn Leu
 340 345 350
 Ser Trp Thr Gly Asn Arg Gly Phe Ile Ser Val Ala Gly Phe Ser Arg
 355 360 365
 Phe Leu Lys Val Cys Gly Ser Glu Leu Val Arg Leu Glu Leu Ser Cys
 370 375 380
 Ser His Phe Leu Asn Glu Thr Cys Leu Glu Val Ile Ser Glu Met Cys
 385 390 395 400
 Pro Asn Leu Gln Ala Leu Asn Leu Ser Ser Cys Asp Lys Leu Pro Pro
 405 410 415
 Gln Ala Phe Asn His Ile Ala Lys Leu Cys Ser Leu Lys Arg Leu Val
 420 425 430
 Leu Tyr Arg Thr Lys Val Glu Gln Thr Ala Leu Leu Ser Ile Leu Asn
 435 440 445
 Phe Cys Ser Glu Leu Gln His Leu Ser Leu Gly Ser Cys Val Met Ile
 450 455 460
 Glu Asp Tyr Asp Val Ile Ala Ser Met Ile Gly Ala Lys Cys Lys Lys
 465 470 475 480
 Leu Arg Thr Leu Asp Leu Trp Arg Cys Lys Asn Ile Thr Glu Asn Gly
 485 490 495
 Ile Ala Glu Leu Ala Ser Gly Cys Pro Leu Leu Glu Glu Leu Asp Leu
 500 505 510
 Gly Trp Cys Pro Thr Leu Gln Ser Ser Thr Gly Cys Phe Thr Arg Leu
 515 520 525
 Ala His Gln Leu Pro Asn Leu Gln Lys Leu Phe Leu Thr Ala Asn Arg
 530 535 540
 Ser Val Cys Asp Thr Asp Ile Asp Glu Leu Ala Cys Asn Cys Thr Arg
 545 550 555 560
 Leu Gln Gln Leu Asp Ile Leu Gly Thr Arg Met Val Ser Pro Ala Ser
 565 570 575
 Leu Arg Lys Leu Leu Glu Ser Cys Lys Asp Leu Ser Leu Leu Asp Val
 580 585 590
 Ser Phe Cys Ser Gln Ile Asp Asn Arg Ala Val Leu Glu Leu Asn Ala
 595 600 605
 Ser Phe Pro Lys Val Phe Ile Lys Lys Ser Phe Thr Gln
 610 615 620

<210> 57
 <211> 984
 <212> DNA
 <213> Homo sapiens

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<400> 57
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tcctacttcc agcagcaact cacatttcag gagtctgtgc ttaaactgtg tcagcctgag 180
cttgagagca gtcagattca catatcagtg ctgccaatgg aggtcctgat gtacatcttc 240
cgatgggttg tgtctagtga cttggacctc agatcattgg agcagttgtc gctgggtgtgc 300
agaggattct acatctgtgc cagagaccct gaaatatggc gtctggcctg cttgaaagtt 360
tggggcagaa gctgtattaa acttggttccg tacacgtcct ggagagagat gtttttagaa 420
cggcctcggtg ttcggtttgga tggcgtgtat atcagtaaaa ccacatatat tcgtcaaggg 480
gaacagtctc ttgatgggtt ctatagagcc tggcaccaag tggaaatatta caggtacata 540
agattctttc ctgatggcca tgtgatgatg ttgacaaccc ctgaagagcc tcagtcatt 600
gttccacgtt taagaactag gaataccagg actgatgcaa ttctactggg tcactatcgc 660
ttgtcacaag acacagacaa tcagaccaa gtatttgctg taataactaa gaaaaaagaa 720
gaaaaaccac ttgactataa atacagatat ttctgtcgtg tccctgtaca agaagcagat 780
cagagttttc atgtggggct acagctatgt tccagtgggc accagaggtt caacaaactc 840
atctggatac atcattcttg tcacattact taaaaatcaa ctggtgagac tgcagtcagt 900
gcttttgaga ttgacaagat gtacaccccc ttgttcttcg ccagagtaag gagctacaca 960
gctttctcag aaaggcctct gtag 984

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<210> 58
<211> 327
<212> PRT
<213> Homo sapiens

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<400> 58
Met Gln Leu Val Pro Asp Ile Glu Phe Lys Ile Thr Tyr Thr Arg Ser
  1             5             10             15

Pro Asp Gly Asp Gly Val Gly Asn Ser Tyr Ile Glu Asp Asn Asp Asp
          20             25             30

Asp Ser Lys Met Ala Asp Leu Leu Ser Tyr Phe Gln Gln Gln Leu Thr
  35             40             45

Phe Gln Glu Ser Val Leu Lys Leu Cys Gln Pro Glu Leu Glu Ser Ser
  50             55             60

Gln Ile His Ile Ser Val Leu Pro Met Glu Val Leu Met Tyr Ile Phe
  65             70             75             80

Arg Trp Val Val Ser Ser Asp Leu Asp Leu Arg Ser Leu Glu Gln Leu
          85             90             95

Ser Leu Val Cys Arg Gly Phe Tyr Ile Cys Ala Arg Asp Pro Glu Ile
          100             105             110

Trp Arg Leu Ala Cys Leu Lys Val Trp Gly Arg Ser Cys Ile Lys Leu
          115             120             125

Val Pro Tyr Thr Ser Trp Arg Glu Met Phe Leu Glu Arg Pro Arg Val
          130             135             140

Arg Phe Asp Gly Val Tyr Ile Ser Lys Thr Thr Tyr Ile Arg Gln Gly
          145             150             155             160

Glu Gln Ser Leu Asp Gly Phe Tyr Arg Ala Trp His Gln Val Glu Tyr
          165             170             175

Tyr Arg Tyr Ile Arg Phe Phe Pro Asp Gly His Val Met Met Leu Thr
          180             185             190

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Thr Pro Glu Glu Pro Gln Ser Ile Val Pro Arg Leu Arg Thr Arg Asn
 195 200 205
 Thr Arg Thr Asp Ala Ile Leu Leu Gly His Tyr Arg Leu Ser Gln Asp
 210 215 220
 Thr Asp Asn Gln Thr Lys Val Phe Ala Val Ile Thr Lys Lys Lys Glu
 225 230 235 240
 Glu Lys Pro Leu Asp Tyr Lys Tyr Arg Tyr Phe Arg Arg Val Pro Val
 245 250 255
 Gln Glu Ala Asp Gln Ser Phe His Val Gly Leu Gln Leu Cys Ser Ser
 260 265 270
 Gly His Gln Arg Phe Asn Lys Leu Ile Trp Ile His His Ser Cys His
 275 280 285
 Ile Thr Tyr Lys Ser Thr Gly Glu Thr Ala Val Ser Ala Phe Glu Ile
 290 295 300
 Asp Lys Met Tyr Thr Pro Leu Phe Phe Ala Arg Val Arg Ser Tyr Thr
 305 310 315 320
 Ala Phe Ser Glu Arg Pro Leu
 325

<210> 59
 <211> 765
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> all n positions
 <223> n=a, c, g or t

<400> 59
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 catgcaaatc catatgttct ccgagctttt gaagacttta gaaagttctc tgagcaagat 120
 gattctgtag agcgagatat aattttacag tgtagagaag gtgaacttgt acttccggat 180
 ttggaaaaag atgatatgat tggtcgccga atcccagcac agaagaaaga agtgccgctg 240
 tctggggccc cagatagata ccaccagtc ccttttcccg aaccctggac tcttcctcca 300
 gaaattcaag caaaatttct ctgtgtactt gaaaggacat gcccatccaa agaaaaaagt 360
 aatagctgta gaatattagt tccttcatat cggcagaaga aagatgacat gctgacacgt 420
 aagattcagt cctggaaact gggaactacc gtgcctccca tcagtttcac ncctggcccc 480
 tgcagtgagg ctgacttgaa gagatgggag gccatccggg aggccagcag actcaggcac 540
 aagaaaaggc tgatggtgga gagactcttt caaaagattt atggtgagaa tgggagtaag 600
 tccatgagtg atgtcagcgc agaagatggt caaaacttgc gtcagctgcg ttacgaggag 660
 atgcagaaaa taaaatcaca attaaaagaa caagatcaga aatggcagga tgaccttgca 720
 aaatggaaaag atcgtcgaaa aagttacact tcagatctgc agaag 765

<210> 60
 <211> 255
 <212> PRT
 <213> Homo sapiens

<400> 60
 Ala Ala Leu Asp Pro Asp Leu Glu Asn Asp Asp Phe Phe Val Arg Lys

1	5	10	15
Thr Gly Ala	Phe His Ala Asn Pro Tyr Val Leu Arg Ala Phe Glu Asp		
	20	25	30
Phe Arg Lys Phe Ser Glu Gln Asp Asp Ser Val Glu Arg Asp Ile Ile			
	35	40	45
Leu Gln Cys Arg Glu Gly Glu Leu Val Leu Pro Asp Leu Glu Lys Asp			
	50	55	60
Asp Met Ile Val Arg Arg Ile Pro Ala Gln Lys Lys Glu Val Pro Leu			
	65	70	75
Ser Gly Ala Pro Asp Arg Tyr His Pro Val Pro Phe Pro Glu Pro Trp			
	85	90	95
Thr Leu Pro Pro Glu Ile Gln Ala Lys Phe Leu Cys Val Leu Glu Arg			
	100	105	110
Thr Cys Pro Ser Lys Glu Lys Ser Asn Ser Cys Arg Ile Leu Val Pro			
	115	120	125
Ser Tyr Arg Gln Lys Lys Asp Asp Met Leu Thr Arg Lys Ile Gln Ser			
	130	135	140
Trp Lys Leu Gly Thr Thr Val Pro Pro Ile Ser Phe Thr Pro Gly Pro			
	145	150	155
Cys Ser Glu Ala Asp Leu Lys Arg Trp Glu Ala Ile Arg Glu Ala Ser			
	165	170	175
Arg Leu Arg His Lys Lys Arg Leu Met Val Glu Arg Leu Phe Gln Lys			
	180	185	190
Ile Tyr Gly Glu Asn Gly Ser Lys Ser Met Ser Asp Val Ser Ala Glu			
	195	200	205
Asp Val Gln Asn Leu Arg Gln Leu Arg Tyr Glu Glu Met Gln Lys Ile			
	210	215	220
Lys Ser Gln Leu Lys Glu Gln Asp Gln Lys Trp Gln Asp Asp Leu Ala			
	225	230	235
Lys Trp Lys Asp Arg Arg Lys Ser Tyr Thr Ser Asp Leu Gln Lys			
	245	250	255

<210> 61
 <211> 36
 <212> PRT
 <213> Homo sapiens

<400> 61
 Leu Pro Pro Glu Leu Ser Phe Thr Ile Leu Ser Tyr Leu Asn Ala Thr
 1 5 10 15
 Asp Leu Cys Leu Ala Ser Cys Val Trp Gln Asp Leu Ala Asn Asp Glu
 20 25 30
 Leu Leu Trp Gln

<210> 62
 <211> 42
 <212> PRT
 <213> Homo sapiens

<400> 62
 Leu Pro Gly Glu Val Leu Glu Tyr Ile Leu Cys Cys Gly Ser Leu Thr
 1 5 10 15
 Ala Ala Asp Ile Gly Arg Val Ser Ser Thr Cys Arg Arg Leu Arg Glu
 20 25 30
 Leu Cys Gln Ser Ser Gly Lys Val Trp Lys
 35 40

<210> 63
 <211> 44
 <212> PRT
 <213> Homo sapiens

<400> 63
 Leu Ala Glu Val Val Glu Arg Val Leu Thr Phe Leu Pro Ala Lys Ala
 1 5 10 15
 Leu Leu Arg Val Ala Cys Val Cys Arg Leu Trp Arg Glu Cys Val Arg
 20 25 30
 Arg Val Leu Arg Thr His Arg Ser Val Thr Trp Ile
 35 40

<210> 64
 <211> 39
 <212> PRT
 <213> Homo sapiens

<400> 64
 Leu Pro Asp Glu Val Val Leu Lys Ile Phe Ser Tyr Leu Leu Glu Gln
 1 5 10 15
 Asp Leu Cys Arg Ala Ala Cys Val Cys Lys Arg Phe Ser Glu Leu Ala
 20 25 30
 Asn Asp Pro Asn Leu Trp Lys
 35

<210> 65
 <211> 41
 <212> PRT
 <213> Homo sapiens

<400> 65
 Leu Pro Leu Glu Leu Trp Arg Met Ile Leu Ala Tyr Leu His Leu Pro
 1 5 10 15
 Asp Leu Gly Arg Cys Ser Leu Val Cys Arg Ala Trp Tyr Glu Leu Ile

	20	25	30
Leu Ser Leu Asp Ser Thr Arg Trp Arg			
	35	40	

<210> 66
 <211> 39
 <212> PRT
 <213> Homo sapiens

<400> 66			
Leu Pro Thr Asp Pro Leu Leu Leu Ile Leu Ser Phe Leu Asp Tyr Arg			
1	5	10	15

Asp Leu Ile Asn Cys Cys Tyr Val Ser Arg Arg Leu Ser Gln Leu Ser			
	20	25	30

Ser His Asp Pro Leu Trp Arg	
	35

<210> 67
 <211> 40
 <212> PRT
 <213> Homo sapiens

<400> 67			
Leu Pro Glu Pro Leu Leu Leu Arg Val Leu Ala Ala Leu Pro Ala Ala			
1	5	10	15

Glu Leu Val Gln Ala Cys Arg Leu Val Cys Leu Arg Trp Lys Glu Leu		
	20	30

Val Asp Gly Ala Pro Leu Trp Leu	
	35 40

<210> 68
 <211> 40
 <212> PRT
 <213> Homo sapiens

<400> 68			
Leu Phe Pro Pro Glu Leu Val Glu His Ile Ile Ser Phe Leu Pro Val			
1	5	10	15

Arg Asp Leu Val Ala Leu Gly Gln Thr Cys Arg Tyr Phe His Glu Val		
	20	30

Cys Asp Gly Glu Gly Val Trp Arg	
	35 40

<210> 69
 <211> 44
 <212> PRT
 <213> Homo sapiens

<400> 69	
Leu Pro Glu Val Leu Leu Leu His Met Cys Ser Tyr Leu Asp Met Arg	

1 5 10 15
Ala Leu Gly Arg Leu Ala Gln Val Tyr Arg Trp Leu Trp His Phe Thr
20 25 30

Asn Cys Asp Leu Leu Arg Arg Gln Ile Ala Trp Ala
35 40

<210> 70
<211> 40
<212> PRT
<213> Homo sapiens

<400> 70
Leu Pro Leu His Met Leu Asn Asn Ile Leu Tyr Arg Phe Ser Asp Gly
1 5 10 15

Trp Asp Ile Ile Thr Leu Gly Gln Val Thr Pro Thr Leu Tyr Met Leu
20 25 30

Ser Glu Asp Arg Gln Leu Trp Lys
35 40

<210> 71
<211> 39
<212> PRT
<213> Homo sapiens

<400> 71
Leu Pro Asp His Ser Met Val Gln Ile Phe Ser Phe Leu Pro Thr Asn
1 5 10 15

Gln Leu Cys Arg Cys Ala Arg Val Cys Arg Arg Trp Tyr Asn Leu Ala
20 25 30

Trp Asp Pro Arg Leu Trp Arg
35

<210> 72
<211> 44
<212> PRT
<213> Homo sapiens

<400> 72
Ile Pro Leu Glu Ile Leu Val Gln Ile Phe Gly Leu Leu Val Ala Ala
1 5 10 15

Asp Gly Pro Met Pro Phe Leu Gly Arg Ala Ala Arg Val Cys Arg Arg
20 25 30

Trp Gln Glu Ala Ala Ser Gln Pro Ala Leu Trp His
35 40

<210> 73
<211> 39
<212> PRT
<213> Homo sapiens

<400> 73
 Leu Pro Pro Glu Val Met Leu Ser Ile Phe Ser Tyr Leu Asn Pro Gln
 1 5 10 15
 Glu Leu Cys Arg Cys Ser Gln Val Ser Met Lys Trp Ser Gln Leu Thr
 20 25 30
 Lys Thr Gly Ser Leu Trp Lys
 35

<210> 74
 <211> 39
 <212> PRT
 <213> Homo sapiens

<400> 74
 Leu Pro Lys Glu Leu Leu Leu Arg Ile Phe Ser Phe Leu Asp Ile Val
 1 5 10 15
 Thr Leu Cys Arg Cys Ala Gln Ile Ser Lys Ala Trp Asn Ile Leu Ala
 20 25 30
 Leu Asp Gly Ser Asn Trp Gln
 35

<210> 75
 <211> 48
 <212> PRT
 <213> Homo sapiens

<400> 75
 Leu Pro Tyr Glu Leu Ile Gln Leu Ile Leu Asn His Leu Thr Leu Pro
 1 5 10 15
 Asp Leu Cys Arg Leu Ala Gln Thr Cys Lys Leu Leu Ser Gln His Cys
 20 25 30
 Cys Asp Pro Leu Gln Tyr Ile His Leu Asn Leu Gln Pro Tyr Trp Ala
 35 40 45

<210> 76
 <211> 44
 <212> PRT
 <213> Homo sapiens

<400> 76
 Leu Pro Met Glu Val Leu Met Tyr Ile Phe Arg Trp Val Val Ser Ser
 1 5 10 15
 Asp Leu Asp Leu Arg Ser Leu Glu Gln Leu Ser Leu Val Cys Arg Gly
 20 25 30
 Phe Tyr Ile Cys Ala Arg Asp Pro Glu Ile Trp Arg

35

40

<210> 77
 <211> 49
 <212> PRT
 <213> Homo sapiens

<400> 77
 Leu Pro Pro Glu Ile Gln Ala Lys Phe Leu Cys Val Leu Glu Arg Thr
 1 5 10 15
 Cys Pro Ser Lys Glu Lys Ser Asn Ser Cys Arg Ile Leu Val Pro Ser
 20 25 30
 Tyr Arg Gln Lys Lys Asp Asp Met Leu Thr Arg Lys Ile Gln Ser Trp
 35 40 45

Lys

<210> 78
 <211> 39
 <212> PRT
 <213> Homo sapiens

<400> 78
 Leu Pro His His Val Val Leu Gln Ile Phe Gln Tyr Leu Pro Leu Leu
 1 5 10 15
 Asp Arg Ala Cys Ala Ser Ser Val Cys Arg Arg Trp Asn Glu Val Phe
 20 25 30
 His Ile Ser Asp Leu Trp Arg
 35

<210> 79
 <211> 43
 <212> PRT
 <213> Homo sapiens

<400> 79
 Leu Trp Ala Trp Gly Glu Lys Gly Val Leu Ser Asn Ile Ser Ala Leu
 1 5 10 15
 Thr Asp Leu Gly Gly Leu Asp Pro Val Trp Leu Val Cys Gly Ser Trp
 20 25 30
 Arg Arg His Val Gly Ala Gly Leu Cys Trp Ala
 35 40

<210> 80
 <211> 59
 <212> DNA
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<220>
 <223> Description of Artificial Sequence:

Oligonucleotide

<400> 80
agtagtaaca aagggtcaaag acagttgact gtatcgtcga ggatgccttc aattaagtt 59

<210> 81
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 81
gcggttactt acttagagct cgacgtctta cttacttagc tcacttctct tcacacca 58

<210> 82
<211> 12
<212> PRT
<213> Homo sapiens

<400> 82
Cys Asp Gly Glu Lys Asp Thr Tyr Ser Tyr Leu Ala
1 5 10

<210> 83
<211> 25
<212> PRT
<213> Homo sapiens

<400> 83
Cys Glu Ser Ser Phe Ser Leu Asn Met Asn Phe Ser Ser Lys Arg Thr
1 5 10 15

Lys Phe Lys Ile Thr Thr Ser Met Gln
20 25

<210> 84
<211> 12
<212> PRT
<213> Homo sapiens

<400> 84
Cys Glu Glu Ala Gln Val Arg Lys Glu Asn Gln Trp
1 5 10

<210> 85
<211> 19
<212> PRT
<213> Homo sapiens

<220>
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<222> 8
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<400> 85

Asn Ala Gly Ser Val Glu Gln Thr Pro Lys Lys Pro Gly Leu Arg Arg
 1 5 10 15

Arg Gln Thr

<210> 86
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 86
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<210> 87
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 87
 ggcttcgagg catttag 17

<210> 88
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 88
 catctggcac gattcca 17

<210> 89
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 89
 ccgctcatcg tatgaca 17

<210> 90
 <211> 19
 <212> PRT
 <213> Homo sapiens

<220>

<221> Phosphorylation
<222> 8
<223> Phosotyrosine

<400> 90
Ala Glu Ile Gly Val Gly Ala Tyr Gly Thr Val Tyr Lys Ala Arg Asp
1 5 10 15

Pro His Ser

<210> 91
<211> 20
<212> PRT
<213> Homo sapiens

<220>
<221> Phosphorylation
<222> 9
<223> Phosothreonine

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<400> 91
Asn Asn Ala Gly Ser Val Glu Trp Thr Pro Lys Lys Pro Gly Leu Arg
1 5 10 15
Arg Arg Gln Thr
20

<210> 92
<211> 15
<212> PRT
<213> Homo sapiens

<400> 92
Gln Ile Tyr Tyr Ser Asp Lys Asp Asp Glu Glu Phe Glu Tyr Arg
1 5 10 15